

Figure 1A

1 CAAGCACTGTGCTAAAGTGTTTTTCATATGTCATGAAAAGTTGTGCCAGAAAATTATGGT 60

61 TTGAACATGGGCAGTTTTCTCCTACCGTCAGCTATATCCACAAGCATCACATGAAGTGG 120

121 GATCTGGCAGCTCTGTGTATTTTCAGTCAAGTTCCACAATGAAACCTGACAATAATGGTAA 180

181 AAACCAATACGGACATCTGAGTAACTGGGGAATTGGCCTGCCTTGCATGTGAGCTTGATG 240

241 GAAGATTGGATATAGACGAGTTGATTATATTTTATGAAGTAGCAGCTCACTACCATCCAC 300

301 CATCCAGGGTTTAAACTACTTTTTTCAGCATCACTTCACCTGTGGACTCTTATACATTTTG 360

361 ATTTCTTGGGGGAAAAATACTGGGATAAGAGGAGGTCATTTTTTAATAAGTTAGCATCCT 420

421 TTTCCCTTTCTTACAAGTTGATCCAAAGGATAAGGCTGTGACTCCATTGGATTGCACCTT 480

481 TAAATCAAAATAGCAGCAGCAGAAGAAAGGGACAATGGCTCTGAGTGGAACTGTAGTCG 540  
 1 M A L S G N C S R 9

541 TTATTATCCTCGAGAACAAGGGTCCGCAGTTCCCAACTCCTTCCCTGAGGTGGTAGAGCT 600  
 10 Y Y P R E Q G S A V P N S F P E V V E L 29

601 GAATGTCGGGGGTCAAGTTTATTTTACTCGCCATTCCACATTGATAAGCATCCCTCATTC 660  
 30 N V G G Q V Y F T R H S T L I S I P H S 49

661 CCTCCTGTGGAAATGTTTTCCCCAAAGAGAGACACGGCTAATGATCTAGCCAAGGACTC 720  
 50 L L W K M F S P K R D T A N D L A K D S 69

721 CAAGGGAAGGTTTTTCATTGACAGAGATGGATTCTTGTTCCGTTATATTCTGGACTATCT 780  
 70 K G R F F I D R D G F L F R Y I L D Y L 89

781 CAGGGACAGGCAGGTGGTCTGCCTGATCACTTTCAGAAAAAGGAAGACTGAAAAGGGA 840  
 90 R D R Q V V L P D H F P E K G R L K R E 109

841 AGCTGAATACTTCCAGCTCCCAGACTTGGTCAAACCTCTGACCCCCGATGAAATCAAGCA 900  
 110 A E Y F Q L P D L V K L L T P D E I K Q 129

901 AAGCCCAGATGAATTCTGCCACAGTGACTTTGAAGATGCCTCCCAAGGAAGCGACACAAG 960  
 130 S P D E F C H S D F E D A S Q G S D T R 149

961 AATCTGCCCCCTTCTCCTGCTCCCTGCCGACCGCAAGTGGGGTTTCATTACTGTGGG 1020  
 150 I C P P S S L L P A D R K W G F I T V G 169

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Figure 1B

1021 TTACAGAGGATCCTGCACCTTGGGCAGAGAGGGACAGGCAGATGCCAAGTTTTCGGAGAGT 1080  
 170 Y R G S C T L G R E G Q A D A K F R R V 189

1081 TCCCCGATTTTGGTTTGTGGAAGGATTTCTTGGCAAAAGAAGTCTTTGGAGAAACTTT 1140  
 190 P R I L V C G R I S L A K E V F G E T L 209

1141 GAATGAAAGCAGAGACCCTGATCGAGCCCCAGAAAGATACACCTCCAGATTTTATCTCAA 1200  
 210 N E S R D P D R A P E R Y T S R F Y L K 229

1201 ATTCAAGCACCTGGAAAGGGCTTTTGATATGTTGTCTCAGAGTGTGGATTCCACATGGTGGC 1260  
 230 F K H L E R A F D M L S E C G F H M V A 249

1261 CTGTAACCTCATCGGTGACAGCATCTTTCATCAACCAATATACAGATGACAAGATCTGGTC 1320  
 250 C N S S V T A S F I N Q Y T D D K I W S 269

1321 AAGCTACACTGAATATGTCTTCTACCGTGAGCCTTCCAGATGGTCACCCTCACACTGCGA 1380  
 270 S Y T E Y V F Y R E P S R W S P S H C D 289

1381 TTGCTGCTGCAAGAATGGCAAAGGTGACAAAGAAGGGGAGAGCGGCACGTCTTGCAATGA 1440  
 290 C C C K N G K G D K E G E S G T S C N D 309

1441 CCTCTCCACATCTAGCTGCGACAGCCAGTCTGAGGCCAGTCTCCCCAGGAGACGGTCAT 1500  
 310 L S T S S C D S Q S E A S S P Q E T V I 329

1501 CTGTGGTCCCCTGACACGCCAGACCAACATCCAGACTCTGGACCGTCCCATCAAGAAGGG 1560  
 330 C G P V T R Q T N I Q T L D R P I K K G 349

1561 CCCTGTCCAGCTGATCCAACAGTCAGAGATGCGGCGGAAAAGCGACTTACTCCGGATTCT 1620  
 350 P V Q L I Q Q S E M R R K S D L L R I L 369

1621 GACTTCAGGCTCCAGGGAATCGAACATGAGCAGCAAAAAAAAAAGCTGTTAAAGAAAAGCT 1680  
 370 T S G S R E S N M S S K K K A V K E K L 389

1681 CTCAATTGAGGAGGAGCTGGAGAAATGTATCCAGGATTTCTTAAAAAAAAAAATTCAGA 1740  
 390 S I E E E L E K C I Q D F L K K K I P D 409

1741 TCGGTTTCTGAGAGAAAACATCCTTGGCAATCTGAACTTTTAAGGAAGTATCATCTATA 1800  
 410 R F P E R K H P W Q S E L L R K Y H L 428

1801 AGGGAGGGCTGGGGCGGGGAAAAAAAAAAAAAGAGTCATTTTGAAATTAACCTCATAA 1860

1861 AAGGAATTCATATTTTAAAGGAAAAAATACAACATAATGATGCACATTTCTTAGAACACA 1920

1921 ATAGTCCATTGATATACTACTGCCTACTTTACCTAGTTCACCTTAACATGTAAATCCACA 1980

Figure 1C

1981 GGGTAGATTTCCTTCTAGATGTGGAAGTACAAGAAAATCTTTTTTAGTTATTTGTTTGT 2040  
 2041 TACTTCGTCCCATGTGCTAACTATCTTATATATAATGAGAGCCAGCTACGTAAAAGTAGC 2100  
 2101 TGAGAGGCCTTGGGAGTCATTTATCCCAAAC TGGGTTTTTCTCTCATCCTTCTACCTCC 2160  
 2161 CTCCTTTGAATGAGGGTATGGTAGAAAAAGATCTGGCCCAATGGCATAAGTTTGAATTT 2220  
 2221 TTAATTTTGGTTTTTTCCTTTTGTATGGGGTTGGGGGAATGGCAGATTTATATGACTT 2280  
 2281 TTCACTCAAATCTATATGTGCCAGTTTATATTGACTCCGTATGCATGAGTATTTGTGCAA 2340  
 2341 CACAAGCACAAC TAAGTATGTATATACACATGACGCACACGATGCCAGGGCCTAGACCTC 2400  
 2401 CCAAGGGCTGTGCTCCTGCTCCAGCAGCCCTCTCTTAGAATATTT CAGATGGATGAGCT 2460  
 2461 TCTGACTCTTTCTTAAATTCCTTTTGGGAAGATTTCC CAGCCTTTCTTCACAACACTTTC 2520  
 2521 TAACATCAAATGACTCTCATCATCAACAAATTGTATTCCTTATTGTGAAATTAATACCCT 2580  
 2581 CAGGCTCCATTTTACTGCTTTGCTCTTTGTCTGCATTAAGAGAGGATGAGGAGAGCTGGT 2640  
 2641 CAAACATTCTTGTGTTAAAAAATCAAACATTCATATCCACAAAATTTTCTGCTAAATG 2700  
 2701 ACTCCACACTCAGCCTTCTCTACCCTGAACTGAATTATCACCCCTTTTCTCCATGTTTTCA 2760  
 2761 GAGTTCTTACTGCCCACAGTTTAAATGGTGTGGCCTTTCCACATAATCCACATTAAGTTCT 2820  
 2821 GTGTTCTGTGTTGTTGTGGAAC TAAGACAACACACAGTACTTGAATAAGGGTCCGGCC 2880  
 2881 TTTTGTGTTGTTT TAGAGAAAGTTGTATTCCACACACAACCTAATAATTTCTTATAAAAAT 2940  
 2941 TTTAAACTACAAAGCTACATTTT TACTTGCTTGTAGCCGTTTTTGTGTTGCCTTTGGGATT 3000  
 3001 CGGGCTTTGGCTGTGCCCATGCTAGGATTTAGCTGTGTCTATTTTATGATGTCTGTAACA 3060  
 3061 ACCCAACAAGGTAAC TGAAGCTCCAGAGTTAAGGTTTCAGATTTCTAAATGAAACTATCT 3120  
 3121 TTTTCAATTACATCCTGACTTGTATAGACACAGCCAAAAAGAACTGTTAATAGCCATCC 3180

105534 6149  
 204279 439507

**Figure 1D**

3181 GTCCATGTAACCTCTGTATTTTACTAAGGTACCAATAGCTCTTTCATAGACTTGTGCTACA 3240  
3241 AGAAGGTTAAAAGACCAGTTTATTTTCAGCATTCCTCATGCATTTTCAGTGGTAACCAAA 3300  
3301 AAATAATTTGTCAATTAATAGTTGTGTGCCAAGCACTCCTAATTTGTTTATTGCGTGTG 3360  
3361 TGTGCATGTGTGTATGTGTATCACAGGTAATAAAGGCAATTGGATGATTAAAAAAAAAA 3420  
3421 AA 3468

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Figure 2A

1			50
K+betaM2	(1)	-----MALSGNCSRYYPREQSAVPNSHPEVVELNVGGQVYFTRHSTIIIS	
AAF558201	(1)	-----MPEIIELNVGGVSYTTILATLLO	
CAA20329.1	(1)	-----MTSVEDVITLNVGGTMYTTIRSTLSK	
Y34129	(1)	-----MDNGDWGYMTDPVTLNVGCHLYTTSLTLTK	
Y34125	(1)	MSRPLITRSPASPLXNQGIPTPAQLTKSNAPVHIVGCHLYTSSLATLTK	
		51	100
K+betaM2	(46)	IPHSLLWKMFSK--KRDANDLAKDSKGRFFIDRDGFLERYITDYLDRQ	
AAF558201	(24)	DKSTLLAEELFG-----EGRDSLAKDSKGRYFFIDRDGVLERYITDFLRDKA	
CAA20329.1	(27)	ETDILLANLASGSLSEDEQANVVTLPDGTLEFIDRDGPLEAVVLFHFLRTDK	
Y34129	(33)	YPSMLCAMEFGG-----D--FPIARDPOGNYFFIDRDGPLERYVILNFLTSE	
Y34125	(51)	YPSRLGRIFDG-----T-EPIVLDSLKHQHYFFIDRDGOMERYITNFLTSTK	
		101	150
K+betaM2	(94)	VVLPHDFPEKGRLLKREAFYFQLPDLVKLLTPDEIKQSPDEFCHSDFEDAS	
AAF558201	(69)	LHLPEGFRERQRLLPEAHHFKLTAMLECRSERDAR-----	
CAA20329.1	(77)	LSLPEQFREVARLKDEADFYRLERSTLLSNASSIS-PRPR-----	
Y34129	(77)	LTLPLDFKEFDLLRKEADFYQLLEPLIQCLNDPKPLY-----	
Y34125	(96)	LLIPDDFKDYTLLYEEAKYFQLQPMLEMERWQDR-----	
		151	200
K+betaM2	(144)	QGSDFRICPPSSLLPADRWGFIITGYRGSCITLGRGQADAKFRVPRIL	
AAF558201	(105)	-----PP---GCITLGYRGSFQFGKGLADVKFRKLSRIL	
CAA20329.1	(117)	-----TANGYNTITSCAETGGYITLGYRGTFAGFRGQADVKFRKLHRL	
Y34129	(113)	-----PMDTFEEVVELSSTRKLSKYSNPVAVLITQLITTK	
Y34125	(132)	-----ETGRFSRPCECLVVRVAPDLGERITLSGDKSLIEEVF	
		201	250
K+betaM2	(194)	VCGRISLAKEVFGDTLNESTRDPDR-APERYTSRFFYLKFKHLERAFDMLSE	
AAF558201	(137)	VCGRVAQCCEVFGDTLNESTRDPDHGGTDYTSRFFLKHCYIEQAFDNLHD	
CAA20329.1	(162)	VCGRATLCREVFADTLNESTRDPGG--PDGE-----	
Y34129	(149)	VHSLLEGISNYFTKWNKHMMDTRD---CQVSFTFGPCDYHQEVSLEVHLM	
Y34125	(169)	PEIGDVMCNSVNAWNHDSHIVIR-----FPLNGYCHLNSVOVLERLQQ	
		251	300
K+betaM2	(243)	CGHHMVACNSSVTASFIN-----QYTDDKIWSSYTEYVFYREPSRWSPSH	
AAF558201	(187)	HGYRMAGSCGSGTAGSAAEPKPGVDTEENRWNYNEFVFIRD-----	
CAA20329.1	(191)	-----	
Y34129	(196)	EYITKQGFTIRNTRVHHMSERANENTVEHNWTFCLARKTDD-----	
Y34125	(213)	RGEHIVGSCGGVDSSQFSEYVLRRELRTPRVPSVIRIKOEPL-----	
		301	350
K+betaM2	(288)	CDCCCKNGKGDKEGESGTSCNDLSTSSCDSQSEASSPQETVICGPVTRQT	
AAF558201	(229)	-----	
CAA20329.1	(191)	-----	
Y34129	(238)	-----	
Y34125	(257)	-----	
		351	400
K+betaM2	(338)	NIQTLDRPIKKGVPVQLIQQSEMRRKSDLLRILTSGSRESNMSSKKKAVKE	
AAF558201	(229)	-----	
CAA20329.1	(191)	-----	
Y34129	(238)	-----	
Y34125	(257)	-----	

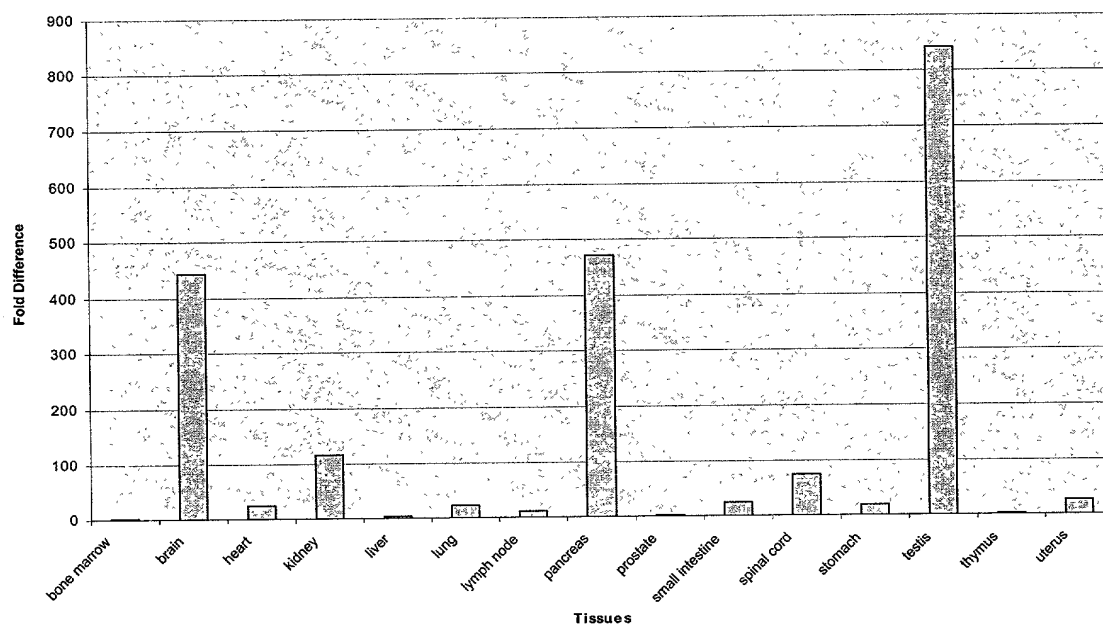
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Figure 2B

	401	441
K+betaM2	(388)	KLSIEEELEKCIQDFLKKKIPDRFPERKHPWQSELLRKYHL
AAF558201	(229)	-----
CAA20329.1	(191)	-----
Y34129	(238)	-----
Y34125	(257)	-----
Consensus	(401)	

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Figure 3



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**Figure 4.**

<b>Protein</b>	<b>Genbank ID</b>	<b>Identities</b>	<b>Similarities</b>
Human potassium channel K+Hnov28	gi Y34129	31%	41%
Drosophila CG10830 protein	gi AAF55820.1	52%	66%
Caenorhabditis K+ channel tetramerisation domain	gi CAA20329.1	42%	51%
Human potassium channel K+Hnov27	gi Y34125	32%	41%

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Figure 5

